

## SEQUENCE LISTING

<110> Rhône-Poulenc Rorer  
 <120> Polypeptides capable of interacting with  
 5 oncogenic mutants of the p53 protein  
 <130> Sequences  
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 <150> FR9812754  
 <151> 1998-10-12  
 15 <160> 33  
 <170> PatentIn Ver. 2.1  
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 20 <211> 23  
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 23  
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<223> Artificial sequence description: 3'-393  
oligonucleotide (p53)

<400> 2  
agatcttcac agtctgagtc aggccttc

29

5

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<212> DNA  
<213> Artificial sequence

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<220>  
<223> Artificial sequence description: 3' H175  
oligonucleotide

<400> 3  
ggggcagtgc ctcac

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15

<210> 4  
<211> 15  
<212> DNA  
<213> Artificial sequence

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<220>  
<223> Artificial sequence description: 3' W248  
oligonucleotide

25

<400> 4  
gggcctccag ttcac

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<211> 15  
<212> DNA  
<213> Artificial sequence

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<220>

<223> Artificial sequence description: 3' H273  
oligonucleotide

<400> 5  
acaaacatgc acctc

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5

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<212> DNA  
<213> Artificial sequence

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<223> Artificial sequence description: 3' G281  
oligonucleotide

<400> 6  
gcgcgggccc ctcac

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15

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<212> DNA  
20 <213> Artificial sequence

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<223> Artificial sequence description: 5'-73  
oligonucleotide

25

<400> 7  
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23

<210> 8  
<211> 1021  
30 <212> DNA  
<213> Artificial sequence

<220>  
<221> CDS

$\langle 222 \rangle \quad (1) \dots (885)$ 

<220>

<223> Artificial sequence description: murine MBP1

5 C-term fragment

$$\begin{array}{llllll} \text{mass} & \text{spring} & \text{damp} & \text{in} & \text{out} & \text{out} \\ \frac{m}{\text{kg}} & \frac{k}{\text{N/m}} & \frac{b}{\text{Ns/m}} & \frac{1}{\text{m}} & \frac{1}{\text{m}} & \frac{1}{\text{m}} \end{array}$$

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 ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg 96  
 Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
 20 25 30  
 cgg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct 144  
 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
 35 40 45  
 aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca 192  
 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
 50 55 60  
 tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt 240  
 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
 65 70 75 80  
 aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc 288  
 Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
 85 90 95  
 gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac 336  
 Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
 100 105 110  
 gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg 384  
 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
 115 120 125  
 gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac 432  
 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His  
 130 135 140  
 caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc 480  
 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
 145 150 155 160  
 tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac 528  
 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp  
 165 170 175  
 aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct 576  
 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
 180 185 190  
 tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg 624  
 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val  
 195 200 205  
 cct gct gac gtg ttt cag atc cag gca acc tct gcc tac cct ggt gcc 672

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Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
210                215                220

tac aat gcc ttt cag acc cgt tct gga aac aca cag ggg gac ttc tac    720
Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
225                230                235                240

att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca    768
Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
245                250                255

gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg    816
Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
260                265                270

aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc    864
Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
275                280                285

ttt gtg gga gcc tat acc ttc tgaagacct cagggaaagg ccacg-gggg    915
Phe Val Gly Ala Tyr Thr Phe
290                295

gccctctccc cctcccatag cttaagcagc cccggggggc tagggatgac cgtctcgtt    975

aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaataa    1021

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- <210> 9
  - <211> 295
  - <212> PRT
  - <213> Artificial sequence
  - <223> Artificial sequence description: murine MBP1 C-term fragment

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20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His  
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp  
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val  
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
275 280 285

Phe Val Gly Ala Tyr Thr Phe  
290 295

<210> 10  
 <211> 39  
 <212> DNA  
 <213> Artificial sequence

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<220>  
 <223> Artificial sequence description: 5' c-myc  
 oligonucleotide

<400> 10  
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39

<210> 11  
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 <212> DNA  
 <213> Artificial sequence

15

<220>  
 <223> Artificial sequence description: 3' c-myc  
 oligonucleotide

<400> 11

20

gattccaggt cctcttcgga gattcagcttc tgctccatg

39

<210> 12

<211> 45

25 <212> DNA

<213> Artificial sequence

<220>

30 <223> Artificial sequence description: 5' MCS  
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<400> 12  
 gatctcggtc gacctgcatg caattcccgg gtgcggccgc gagct

45

<210> 13

35 <211> 37



<212> DNA

<213> Artificial sequence

<220>

5 <223> Artificial sequence description: 3' MCS  
oligonucleotide

<400> 13

cgcgggccgca cccgggaatt gcatgcaggt cgaccga

37

10 <210> 14

<211> 22

<212> DNA

<213> Artificial sequence

15 <220>

<223> Artificial sequence description: 3' mMBP1  
oligonucleotide

<400> 14

cgggtactggc agaggttaact gg

22

20

<210> 15

<211> 1513

<212> DNA

<213> Artificial sequence

25

<220>

<221> CDS

<222> (49)..(1377)

30 <220>

<223> Artificial sequence description: murine MBP1  
(complete sequence)

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Met Leu Pro  
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ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg	105
Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu	
5 10 15	
ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc	153
Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser	
20 25 30 35	
tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac	201
Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His	
40 45 50	
tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt	249
Cys Arg Asp Val Asn Gln Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly	
55 60 65	
gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc	297
Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys Leu Pro Arg	
70 75 80	
tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca	345
Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro	
85 90 95	
gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct	393
Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro	
100 105 110 115	
gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg	441
Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu	
120 125 130	
cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac	489
His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr	
135 140 145	
cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg	537
Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val	
150 155 160	
gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac	585
Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn	
165 170 175	
ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga	633
Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly	
180 185 190 195	
cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc	681
Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala	
200 205 210	
cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc	729
Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg	
215 220 225	
tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat	777
Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp	

230	235	240	
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc			825
Ile Asp Glu Cys Gly Tyr Ser Tyr Leu Cys Gln Tyr Arg Cys Val			
245	250	255	
aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg			873
Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu			
260	265	270	275
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca			921
Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala			
280	285	290	
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac			969
His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Tyr			
295	300	305	
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca			1017
Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser			
310	315	320	
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag			1065
Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln			
325	330	335	
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt			1113
Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser			
340	345	350	355
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt			1161
Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly			
360	365	370	
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc			1209
Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe			
375	380	385	
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg			1257
Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg			
390	395	400	
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc			1305
Pro Val Thr Gly Pro Arg Gln Tyr Val Leu Asp Leu Glu Met Val Thr			
405	410	415	
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg			1353
Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr			
420	425	430	435
gtc ttt gtg gga gcc tat acc ttc tgaagacct caggaaggg ccatgtggg			1407
Val Phe Val Gly Ala Tyr Thr Phe			
440			
gccccctccc cctcccatag cttaagcagc cccggggggcc tagggatgac cgttctgctt			1467
aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaanaa			1513

<210> 16

<211> 443

<212> PRT

<213> Artificial sequence

5 <223> Artificial sequence description: murine MBP1  
(complete sequence)

&lt;400&gt; 16

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 1 5 10 15

Phe Leu Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu  
 20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp  
 35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
 50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
 65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro  
 85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly  
 100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr  
 115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
 130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
 145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
 165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
 180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
 195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
 210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
 225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr  
 245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
 260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
 275 280 285  
 Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
 290 295 300  
 Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val  
 305 310 315 320  
 Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
 325 330 335  
 Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser  
 340 345 350  
 Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
 355 360 365  
 Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln  
 370 375 380  
 Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
 385 390 395 400  
 Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
 405 410 415  
 Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
 420 425 430  
 Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
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<210> 17

<211> 21

5 <212> DNA

<213> Artificial sequence

<220>

10 <223> Artificial sequence description: 3' hMBP1  
oligonucleotide

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21

<210> 18

15 <211> 21

<212> DNA

<213> Artificial sequence

&lt;220&gt;

<223> Artificial sequence description: 5' hMBP1  
oligonucleotide

5

&lt;400&gt; 18

tgtagctact ccagctacct c

21

&lt;210&gt; 19

&lt;211&gt; 1122

10 &lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

<223> Artificial sequence description: human MBP1 cDNA  
(partial sequence)

15

&lt;400&gt; 19

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ctggggatca gcttctcttc aggatcttga agagcccgac agctacatgc aatgcacaga 180
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ccctgaggcc tgcaaggggg aatgaagtg catcaaccac tacggggggct acttgtgcct 300
gccccgtccc gctgccgtca tcaacgacct acacggcgag ggaacccccc caccagtgc 360
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cagtgatatt gatgagtgtg gctactccag ctacctctgt cagtaacctg gcgtcaacga 840
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ccaagacatt gatgagtgtg agctctgtgc gaaccagtgc tccgagggcc aaacctgtgt 960
caacttccat gggggctacc gctgcgtgga caccaaccgc tgcgtggagc cccacatcca 1020
ggctctctgag aaccgtgttc tctgcccggc ctccaaacct ctatgtcgag agcagccttc 1080
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&lt;210&gt; 20

20 &lt;211&gt; 684

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

<223> Artificial sequence description: human MBP1 cDNA  
(partial sequence)

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tgtgagtcctg gtgcgcacca gtgctccgag gcccaaacct gtgtcaactc ccattgggggc 180
taccgctcgtg tggacaccaa ccgctgcgtg gagccctaca tccaggtctc tgagaaccgc 240
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ttttacatta ggcaaatcaa caacgtcagc gccatgctgg tcttcgcccg gccggtgacg 480
ggcccccggt agtacgtgct ggacctggag atggtcacca tgaattccct catgagctac 540
cgggccagct ctgtactgag gctcaccgtc ttgtaggagg cctacacctt ctgaggagca 600
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gagaaaggca ataaaggag aaag 684

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<210> 21

<211> 1480

<212> DNA

10 <213> Artificial sequence

<220>

<221> CDS

<222> (59)..(1387)

15

<220>

<223> Artificial sequence description: human MBP1  
(complete sequence)



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Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15  
ctg cta ctg ttg ctc ttg gga tca gct tct cct cag gat tct gaa gag 154  
Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
20 25 30  
ccc gac agc tac acg gaa tgc aca gat ggc tat gag tgg gac cca gac 202  
Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
35 40 45  
agc cag cac tgc cgg gat gtc aac gag tgt ctg acc atc cct gag gcc 250  
Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60  
tgc aag ggg gaa atg aag tgc atc aac cac tac ggg ggc tac ttg tgc 298  
Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80  
ctg ccc cgc tcc gct gcc gtc atc aac gac cta cac ggc gag gga ccc 346  
Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
85 90 95  
ccg cca cca gtg cct ccc gct caa cac ccc aac ccc tgc cca cca ggc 394  
Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly  
100 105 110  
tat gag ccc gac gat cag gac agc tgt gtg gat gtg gac gag tgt gcc 442  
Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
115 120 125  
cag gcc ctg cac gac tgt cgc ccc agc cag gac tgc cat aac ttg cct 490  
Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140  
ggc tcc tat cag tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc 538  
Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160  
gag tgt gtg gac ata gac gag tgc cgc tac cgc tac tgc cag cac cgc 586  
Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175  
tgc gtg aac ctg cct gcc tcc ttc cgc tgc cag tgc gag ccg gcc ttc 634

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe	
180 185 190	
cag ctg ggg cct aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac	682
Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp	
195 200 205	
atg ggg gcc cca tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc	730
Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe	
210 215 220	
ctg tgt cgc tgc cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc	778
Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser	
225 230 235 240	
cgc agt gat att gat gag tgt agc tac tcc agc tac ctc tgt cag tac	826
Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr	
245 250 255	
cgc tgc gtc aac gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt	874
Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly	
260 265 270	
tac cag ctg ctg gcc aca cgc ctc tgc caa gac att gat gag tgt gag	922
Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu	
275 280 285	
tct ggt gcg cac cag tgc tcc gag gcc caa acc tgt gtc aac ttc cat	970
Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His	
290 295 300	
ggg gcc tac cgc tgc gtg gac acc aac cgc tgc gtg gag ccc tac atc	1018
Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile	
305 310 315 320	
cag gtc tct gag aac cgc tgt ctc tgc ccg gcc tcc aac cct cta tgt	1066
Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys	
325 330 335	
cga gag cag cct tca tcc att gtg cac cgc tac atc gcc atc acc tcg	1114
Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser	
340 345 350	
gag cgg agc gtg ccc gct gac gtg ttc cag atc cag gcg acc tcc gtc	1162
Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val	
355 360 365	
tac ccc ggt gcc tac aat gcc ttt cag atc cgt gct gga aac tcg cag	1210
Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln	
370 375 380	
ggg gac ttt tac att agg caa atc aac aac gtc agc gcc atg ctg gtc	1258
Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val	
385 390 395 400	
ctc gcc cgg ccg gtg acg gcc ccc cgg gag tac gtg ctg gac ctg gag	1306
Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu	
405 410 415	

atg gtc acc atg aat tcc ctc atg agc tac cgg gcc agc tct gta ctg 1354  
 Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
 420 425 430

agg ctc acc gtc ttt gta ggg gcc tac acc ttc tgaggagcag gagggagcca 1407  
 Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
 435 440

ccctccctgc agctacccta gctgaggagc ctgttgtag gggcagaatg agaaaggcaa 1467

taaagggaga aag 1480

<210> 22

5 <211> 443

<212> PRT

<213> Artificial sequence

<223> Artificial sequence description: human MBP1  
 (complete sequence)

&lt;400&gt; 22

Met	Leu	Pro	Cys	Ala	Ser	Cys	Leu	Pro	Gly	Ser	Leu	Leu	Leu	Trp	Ala
1				5					10					15	
Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ser	Ala	Ser	Pro	Gln	Asp	Ser	Glu	Glu
			20					25					30		
Pro	Asp	Ser	Tyr	Thr	Glu	Cys	Thr	Asp	Gly	Tyr	Glu	Trp	Asp	Pro	Asp
		35					40					45			
Ser	Gln	His	Cys	Arg	Asp	Val	Asn	Glu	Cys	Leu	Thr	Ile	Pro	Glu	Ala
		50				55					60				
Cys	Lys	Gly	Glu	Met	Lys	Cys	Ile	Asn	His	Tyr	Gly	Gly	Tyr	Leu	Cys
65					70					75				80	
Leu	Pro	Arg	Ser	Ala	Ala	Val	Ile	Asn	Asp	Leu	His	Gly	Glu	Gly	Pro
				85					90					95	
Pro	Pro	Pro	Val	Pro	Pro	Ala	Gln	His	Pro	Asn	Pro	Cys	Pro	Pro	Gly
			100					105					110		
Tyr	Glu	Pro	Asp	Asp	Gln	Asp	Ser	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala
		115				120						125			
Gln	Ala	Leu	His	Asp	Cys	Arg	Pro	Ser	Gln	Asp	Cys	His	Asn	Leu	Pro
		130				135					140				
Gly	Ser	Tyr	Gln	Cys	Thr	Cys	Pro	Asp	Gly	Tyr	Arg	Lys	Ile	Gly	Pro
145					150					155				160	
Glu	Cys	Val	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Arg	Tyr	Cys	Gln	His	Arg
			165					170					175		
Cys	Val	Asn	Leu	Pro	Gly	Ser	Phe	Arg	Cys	Gln	Cys	Glu	Pro	Gly	Phe
		180					185						190		
Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp
		195				200							205		

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
 210 215 220

Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
 225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr  
 245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
 260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Gly Cys Glu  
 275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
 290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile  
 305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
 325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser  
 340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
 355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln  
 370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
 385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
 405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
 420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
 435 440

<210> 23

5 <211> 817

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: murine MBP1  
cDNA (partial sequence)

<400> 23  
gctgtggcag aaacccctga cttctgccca ccacctccca gcctcaggat gctccctttt 60  
gctctctgcc tccccgggtc tttgtgtctc tgggcgttcc tgcgttgcct cttgggagca 120  
gcgtcccccac aggatcccca ggagccggac agctacacgg aatgcacaga tggctatgag 180  
tgggatgcag acagccagca ctgcgggatc gtcaacgagt gcctgaccat cccggaggct 240  
tgcaaggggtg agatgaaatg catcaaccac tacggggggtt atttgtgtct gccctgcctct 300  
gctgccttca tcagtgatct ccatgggtgaa ggacctccac cgccagcggc ccatgtctca 360  
caaccaaaac cttgcccgcga gggctacgag cctgatgaac agggagctg tgggatgtg 420  
gacgagtcta cccaggcttt gcatgactgt cggcctatgc aggactgcta taacctctct 480  
ggctcctacc agtgcacctg ccttgatggt taccgaaaaa ttggacccga atgtgtggac 540  
atagatgagt gtctttaccg ctatgcccag catcgatgtg tgaacctgcc gggctctttt 600  
cgatgccagt gtgagccagg cttccagttg ggaccttaaca accgctcttg tgtggatgtg 660  
aatgagtgtg acatggggagc ccatgtgag cagcgtctgt tcaactccta tgggaccttc 720  
ctgtgtctgt graaccaggg ctatgagctg caccgggatg gcttctctg cagcgatata 780  
gatgagtgcg gctactccag ttacctctgc cagtacc 817

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<210> 24  
<211> 24  
<212> DNA  
<213> Artificial sequence

10

<220>  
<223> Artificial sequence description: sense-GAPDH  
oligonucleotide

<400> 24  
cggagtcaac ggattgggtc gtaa

24

15

<210> 25  
<211> 24  
<212> DNA  
<213> Artificial sequence

20

<220>  
<223> Artificial sequence description: antisense-GAPDH  
oligonucleotide

25

<400> 25  
agccttctcc atggtgggtga agac

24

<210> 26  
 <211> 25  
 <212> DNA  
 <213> Artificial sequence

5

<220>  
 <223> Artificial sequence description: oligonucleotide

<400> 26  
 cggttggcct tggggttcag ggggg

25

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<210> 27  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence

15

<220>  
 <223> Artificial sequence description: sense MBP1  
 oligonucleotide

<400> 27  
 gccctgatgg ttaccgaag a

21

20

<210> 28  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence

25

<220>  
 <223> Artificial sequence description: antisense MBP1  
 oligonucleotide

30

<400> 28  
 agcccccatg gaagttgaca c

21

<210> 29  
 <211> 20

<212> DNA  
 <213> Artificial sequence

<220>

5 <223> Artificial sequence description: sense-actin  
 oligonucleotide

<400> 29  
 gtggggcgcc ccaggcacca

20

10 <210> 30  
 <211> 1358  
 <212> DNA  
 <213> Artificial sequence

15 <220>  
 <221> CDS  
 <222> (1)..(885)

<220>

20 <223> Artificial sequence description: human MBP1  
 C-term fragment

<400> 30  
 tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgt gtg gac 48  
 Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
 1 5 10 15

ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg 96  
 Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
 20 25 30

cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct 144  
 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
 35 40 45



aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac atg ggg gcc cca 192  
 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
 50 55 60

tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgc 240  
 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
 65 70 75 80

cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc tgc agt gat att 288  
 His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
 85 90 95

gat gag tgt agc tac tcc agc tac ctc tgt cag tac cgc tgc gtc aac 336  
 Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
 100 105 110

gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt tac cag ctg ctg 384  
 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
 115 120 125

gcc aca cgc ctc tgc caa gac att gat gag tgt gag tct ggt gcg cac 432  
 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His  
 130 135 140

cag tgc tcc gag gcc caa acc tgt gtc aac ttc cat ggg ggc tac cgc 480  
 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Tyr Arg  
 145 150 155 160

tgc gtg gac acc aac cgc tgc gtg gag ccc tac atc cag gtc tct gag 528  
 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu  
 165 170 175

aac cgc tgt ctc tgc ccg gcc tcc aac cct cta tgt cga gag cag cct 576  
 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
 180 185 190

tca tcc att gtg cac cgc tac atg acc atc acc tcy gag cgg agc gtg 624  
 Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val  
 195 200 205

ccc gct gac gtg ttc cag atc cag gcg acc tcc gtc tac ccc ggt gcc 672  
 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
 210 215 220

tac aat gcc ttt cag atc cgt gct gga aac tcy cag ggg gac ttt tac 720  
 Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr  
 225 230 235 240

att agg Caa atc aac aac gtc agc gcc atg ctg gtc ctc gcc cgg ccg 768  
 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
 245 250 255

gtg acg ggc ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg 816  
 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
 260 265 270

aat tcc ctc atg agc tac ccg gcc agc tct gta ctg agg ctc acc gtc 864  
 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val

275

280

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ttt gta ggg gcc tac acc ttc tgaggagcag gaggagacca cctccctgc 915  
 Phe Val Gly Ala Tyr Thr Phe  
 290 295

agctacccta gctgaggagc ctgttgtgag gggcagaatg agaaaggcaa taaagggaga 975  
 aagaaagtcc tgggtggctga ggtgggcggg tcacactgca ggaagcctca ggtggggca 1035  
 ggtgggcact tgggggggca ggccaagtcc acctaaatgg gggctctctat atgttcaggc 1095  
 ccaggggccc ccattgacag gagctggggag ctctgcacca cgagcttcag tcaccccgag 1155  
 aggagaggag gtaacgagga gggcggactc caggccccgg ccagagagatt tggacttggc 1215  
 tggcttgacg gggtcctaag aaactccact ctggacagcg ccaggaggcc ctgggttcca 1275  
 ttcctaactc tgctcaaac tgcacatttg gataagccct agtagttccc tgggcctggt 1335  
 tttctataaa acgaggcaac tgg 1358

<210> 31

<211> 295

5 <212> PRT

<213> Artificial sequence

<223> Artificial sequence description: human MBP1

C-term fragment

&lt;400&gt; 31

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
 1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
 20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
 35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
 50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
 65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
 85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
 100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
 115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His  
 130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg

145	150	155	160
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu			
165		170	175
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro			
180	185	190	
Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val			
195	200	205	
Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala			
210	215	220	
Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr			
225	230	235	240
Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro			
245	250	255	
Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met			
260	265	270	
Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val			
275	280	285	
Phe Val Gly Ala Tyr Thr Phe			
290	295		

&lt;210&gt; 32

&lt;211&gt; 1663

&lt;212&gt; DNA

5 &lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(999)

10

&lt;220&gt;

<223> Artificial sequence description: murine fibulin  
2 c-term fragment

&lt;400&gt; 32

gag ggc tct gaa tgc gtg gat gtg aat gag tgc gag aca ggt gtg cat 48  
 Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His  
 1 5 10 15

cgc tgc ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc 96  
 Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg  
 20 25 30

tgc gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc 144  
 Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
 35 40 45

att gat gtg aac gaa tgc tgg gtc tcg ccg ggc cgc ctg tgc cag cac 192  
 Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His

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50	55	60	
aca tgt gag aac	aca cgg ggc tcc	tac cgc tgc tcc	tgc gct gct ggc 240
Thr Cys Glu Asn	Thr Pro Gly Ser	Tyr Arg Cys Ser	Cys Ala Ala Gly
65	70	75	80
ttc ctt ttg gcc	gca gat ggc aaa	cat tgt gaa gat	gtg aac gag tgc 288
Phe Leu Leu Ala	Ala Asp Gly Lys	His Cys Glu Asp	Val Asn Glu Cys
	85	90	95
gag act cgg cgc	tgc agc cag gaa	tgt gcc aac atc	tat ggc tcc tat 336
Glu Thr Arg Arg	Cys Ser Gln Glu	Cys Ala Asn Ile	Tyr Gly Ser Tyr
100	105	110	
cag tgc tac tgc	cgt cag ggc tac	cag ctg gca gag	gat ggg cat acc 364
Gln Cys Tyr Cys	Arg Gln Gly Tyr	Gln Leu Ala Glu	Asp Gly His Thr
115	120	125	
tgc aca gac atc	gat gag tgt gca	cag ggc gcg ggc	att ctc tgt acc 432
Cys Thr Asp Ile	Asp Glu Cys Ala	Gln Gly Ala Gly	Ile Leu Cys Thr
130	135	140	
ttc cgc tgt gtc	aac gtg cct ggg	agc tac cag tgt	gca tgc cca gag 480
Phe Arg Cys Val	Asn Val Pro Gly	Ser Tyr Gln Cys	Ala Cys Pro Glu
145	150	155	160
caa ggg tat aca	atg atg gcc aac	ggg agg tcc tgc	aag gac ctg gat 528
Gln Gly Tyr Thr	Met Met Ala Asn	Gly Arg Ser Cys	Lys Asp Leu Asp
	165	170	175
gag tgt gca ctg	ggc acc cac aac	tgc tct gag gct	gag acc tgc cac 576
Glu Cys Ala Leu	Gly Thr His Asn	Cys Ser Glu Ala	Glu Thr Cys His
180	185	190	
aat atc cag ggg	agt ttc cgc tgc	ctg cgc ttt gat	tgt cca ccc aac 624
Asn Ile Gln Gly	Ser Phe Arg Cys	Leu Arg Phe Asp	Cys Pro Pro Asn
195	200	205	
tat gtc cgt gtc	tca caa acg aag	tgc gag cgc acc	aca tgc cag gat 672
Tyr Val Arg Val	Ser Gln Thr Lys	Cys Glu Arg Thr	Thr Cys Gln Asp
210	215	220	
atc acg gaa tgt	caa acc tca cca	gct cgc atc acg	cac tac cag ctc 720
Ile Thr Glu Cys	Gln Thr Ser Pro	Ala Arg Ile Thr	His Tyr Gln Leu
225	230	235	240
aat ttc cag aca	ggc cta ctg gta	cct gca cat atc	ttc cgc atc ggc 768
Asn Phe Gln Thr	Gly Leu Leu Val	Pro Ala His Ile	Phe Arg Ile Gly
	245	250	255
cct gct ccc gcc	ttt gct ggg gac	acc atc tcc ctg	acc atc acg aag 816
Pro Ala Pro Ala	Phe Ala Gly Asp	Thr Ile Ser Leu	Thr Ile Thr Lys
260	265	270	
ggc aat gag gag	ggc tac ttc gtc	aca cgc aga ctc	aat gcc tac act 864
Gly Asn Glu Glu	Gly Tyr Phe Val	Thr Arg Arg Leu	Asn Ala Tyr Thr
275	280	285	
ggg gtg gta tcc	ctg cag cgg tct	gtt ctg gag ccg	cgg gac ttt gcc 912

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala  
 290 295 300

cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc 960  
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
 305 310 315 320

ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgaggtgaca 1009  
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
 325 330

tgtagcgcaa tccctccagg tgatgectgg gcggtgggca gctgcgccac tccaaagtgg 1069

ctttttctgg tgactctgta acttaactta atcatgctga gctgggttgg cttgagcttc 1129

tacccctagag ggagggagat gcacccccagc aggcactgag tacagggccag ggtcaccga 1189

ggctagatgg tgacctgcaa actggaacaa gccatagggg gcttctgaac tccactcttc 1249

aaactatggct acagctgaca ttccattcct tcatccactg tgttcttcaa ttaaaaaaaa 1309

aaatcagctg tgcattgtag cacagacctt taatcctagc actggggagg cagaggtagg 1369

tagatctctg agttccagcc cagcctgggtc tacactggga gttctaacca gccagagcta 1429

catagagaga ccttatctca acaaggaaaa aacgaaagaa atctctgtga gttccagccc 1489

agcctggctt acgctgggag ttctaaccag ccagagctac atagagagat cctatctcaa 1549

caaggaaaaa tgaagaaaat catcttaaaa gggttttttt ttgtctgttg ttgtttaatg 1609

ataagagtag cacatatata ttattaaaaa tgatcaataa gcacagaaag gta 1663

<210> 33

<211> 333

5 <212> PRT

<213> Artificial sequence

<223> Artificial sequence description: murine fibulin  
 2 c-term fragment

&lt;400&gt; 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His  
 1 5 10 15

Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg  
 20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
 35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His  
 50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly  
 65 70 75 80

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys  
 85 90 95

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Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr  
 100 105 110  
 Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr  
 115 120 125  
 Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr  
 130 135 140  
 Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu  
 145 150 155 160  
 Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp  
 165 170 175  
 Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His  
 180 185 190  
 Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn  
 195 200 205  
 Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp  
 210 215 220  
 Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu  
 225 230 235 240  
 Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly  
 245 250 255  
 Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys  
 260 265 270  
 Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr  
 275 280 285  
 Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala  
 290 295 300  
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
 305 310 315 320  
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
 325 330